

OY		114	EENUNROPOOYOECOSGONHNEPFRIMCOSOORSEVREKEROOKRUYEBOORE	173
Db		110	YEKOQOOORDFOKRFCOSQRCSOMEOBRPERKKOCUACBCEVOEDPWKEGR-----E	160
OY		174	EKYEEEMKBEODNRDPDOOREXEDCSRRCESDOPROOYCQRRCRSEDOROHNGRDLLNPO	233
Db		161	NKWREEEEEEES-----	171
OY		234	RGSRSRYEEEGEKSDNDNYFEDEBSLSTRFTRHEEHISVLNFYFSRLTKLYRVLV	293
Db		172	-DBGBGOQQNNPNPYEFHRKSFDGFEBHEGNFNFLDFADKHHLRGINERLATI	224
OY		294	LEANNAEVLPPLMLPADAILVTGGAGALCKMHNDRNSYNLECCDVIRIPACTFYULIN	353
Db		225	LEANNTFYLPHNCBAEKTYVTNGRGIVTFTPTHKSKSYNVBPVVVRIPAGSVILAN	284
OY		334	RDNMRNLIAKLQTITSPGYCKEFFRPYGOGNPDEYLSSTFKELLDAALNTOAERVGLV	413
Db		285	QNREKLTIALVINHPVNPPNOFOKFEPFPAOEPMDSUYLEIFSRKELLEAVFNTRSOLDDELPR	344
OY		414	G-----QOREGVITSASOEIRELTRDDSSRWMIHNRGEESRG-PYLNFPNKPLYS	465
Db		345	GGROSRRHQOQGGMRKMSQSIEDRALSGATSPR-----GKGSGTAFFNISOTPKXS	397
OY		466	NKYGAUEVEKPREDY-ROLQDMVDVSFIANTIGOSCMMGFETRTSRIKVVAVGAEADVEMA	524
Db		398	NONGRFETYACAPRNFGQOLREVDDSSVVAIEINKSIPEFHYNASKAFPVVLTEGNGHVEMY	457
OY		525	CPIHLGHRRGGRRGGRRHNEBDY-----HYEQKARLSREALTVVHGVPVNVVSSGN	577
Db		458	CPHLS-ROSSOWSMSEEDEQEDEVERSGQVKRAQLSTGNLFVYPAGHPVTYAASON	516
OY		578	ENLLFAFGI-NAONNHENFLAGERNVLOQIDEPAMELAAPARKEYEELSODESIEF	636
Db		517	EDLGTLGLGLYTGQDKKTIFAAGKTNNV-ROMDRQAKELAFGVESRLVDENVNNPOSZY	575
OY		637	PGRPQHOOQSSRSRTRKQOOPVSLIDE	663
Db		576	FVSGRDRKGFDER-RGSNNPLSPFD	601
<hr/>				
RESULT	2			
VCLB_GOSHI	STANDARD:	PRT:	588 AA.	
ID_VCLB_GOSHI	STDARD:	PRT:	588 AA.	
AC	P09801,			
DT	01-MAR-1989 (Rel. 10, Created)			
DT	01-MAR-1989 (Rel. 10, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	VICLIN C72 PRECURSOR (ALPHA-GLOBULIN B).			
OS	Gossypium hirsutum (Upland cotton).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;			
OC	Malvales; Malvaceae; Gossypium.			
RP	[1]			
RA	SCHAN F FROM N.A.			
RA	Chuan C.A., Pyle J.B., Legocki A.B., Dure L. III;			
RT	"Developmental biochemistry of cottonseed embryogenesis and			
RT	germination. XVII. cDNA and amino acid sequences of the members of			
RU	the storage protein families."			
CC	Plant Mol. Biol. 7:475-489(1986).			
CC	-1- FUNCTION: SEED STORAGE PROTEIN.			
CC	-1- SUBCELLULAR LOCATION: CYTOLEMARY MEMBRANE-BOUND VACUOLAR PROTEIN			
CC	BODIES.			
CC	-1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,			
CC	CONVICILLIN, CONGLYCINNIN, ETC.).			
CC	--			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			

CC -----
DR EMBL: M16891: AAA33071.1; -.
DR PIR: A30838; FMCNAB.
DR HSSP: P50477; ICAX.
DR INTERPRO: IPR00113; -.
DR PfAM: PF00546; Seedstore_7s; 1.
KW Seed storage protein; signal.
FT SIGNAL 1 25
FT CHAIN 26 588 VICILIN C72
SQ SEQUENCE 588 AA; 69729 MW; 63B699B29AB8ADEB CRC64;

Query Match	30.7%;	Score 1083.5;	DB 1;	Length 588;
Best Local Similarity	38.2%;	Pred. No. 8.7e-60;		
Matches 229;	Conservative 114;	Mismatches 182;	Indels 75;	Gaps 13

OY	76	DDPQIDCCGCGCRRCKNQESGRPROOYCQRCKEICEEESEENRQR--DPQQYEOQCENG	133
Db	35	DDPRKRYEDCRRCRWDTIRGQKEEQQCESSCYGEKKXOOHRHREDQRRREECQRC	94
OY	134	ORHEPEPHMQTCQQRCEERYEKERKQOKRYEEOUREDEEKYEEMKEDDKRPQOQB	193
Db	95	R-QQEERPPQCGQRLCKRFEGEQDQ-----SQNQ-----	123
OY	194	YEDCRREEODE--PROUYOCQRREDOROHGRLINPOR-----GGSGRIEBEGE	245
Db	124	FQECQHCHQOQREKRKOOCVRECEREQE-----NPMRREBEAEETEESBQO	175
OY	246	KOSDPYFDEFDSLTFRFTTEGHISYLENFGRSKLTLAKNLRYLVLEAPNPAFLPT	305
Db	176	EQSHPHFHHRSPQSRPFREHGNRVLDQRFASRHPLRGILNEFLSLILEANPTFTVLPH	235
OY	306	HLADAILLVYGGRALKMHIHDNRBSYNLECGDVIRIPAGTFFYLINDONNERLIAKF	365
Db	236	HODACKIYLVNGRTLLFTLTHENKESYVVVGVVVRVAVAGSTVYLANDNKELIAVL	295
OY	366	LQTIPTPGYKREFPAGGCPNPETYSFKELLALNALQARLGVLG-----QORE	418
Db	296	HRPVNNPROFEFFFPAGSORPOSTLRATSRLELPATFNTRSDDELFGCSHRHQGOQ	355
OY	419	GVIISAOEQIRELTRDDESRRMHIRGCESSRGPYNLFNKPPLYSNKYGAUYEVKPD	478
Db	356	GMFRASQEQIRALSQEAITSPIR-----EKSGE--RAFNLLYRTPRYSNONGFYEACPRE	409
OY	479	YROLDMQSVYIANITGSMKGPFEPNTIRSTVYVVVASGLADVEAMCAPLSRHHGRRGG	538
Db	410	FRLDLINVTYSALOLNQGSIFVPKNSATFPEVLVINEGNGVEVENSPLLPRQSSFESEE	469
OY	539	KRHEEDEVD-----HYDQVKARKLKREAIIVPCVHPVVFVSNGENMLLPFAFG-----I	587
Db	470	EQQOEDEDEEFERSQYRKIRKSOLRGDLTVVPANFPVTFAVSQNOMLPMTFGLYMONI	529
OY	568	NAQNHNENFLAGRENVLIQOIEPQAMELAFAAPRKREVELDFNSODESJTFFPSRHOQOS	647
Db	530	NPDHMQRIFVAGIKNHV-RQMDSQAKELAFGVSSRLVIDEIFNNNPQESFYFS-RQORRAS	587
RESULT 3			
GLBI_MAIZE			
ID	GLBI_MAIZE	STANDARD;	PRT; 573 AA.
AC	PL5590;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-AUG-1990 (Rel. 15, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	GLOBALIN-1 S ALLELE PRECURSOR (GLBI-S) (75-Like).		
GN	GLBI.		
OS	zea mays (Maize).		
OC	Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; zea.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
SC	STRAIN=CV. INBREDED LINE VA26;		
CA	Belanger F.C., Kriz A.L.;		

	RT	"Molecular characterization of the major maize embryo globulin encoded by the Gbl1 gene."
	RT	Plant Physiol. 91:636-643(1989).
	RN	[2]
	RP	SEQUENCE OF 87-100.
	RX	MEDLINE=89374022; PubMed=2775172;
	RA	Kriz A.L.:
	RT	"Characterization of embryo globulins encoded by the maize Glb genes";
	RL	Biochem. Genet. 27:239-251(1989).
	CC	-I- PPM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE NATIVE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.
	CC	-I- POLYMORPHISMS: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL PROTEINS, RESPECTIVELY.
	CC	-I- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASCOLIN, VICILIN, CONVICILIN, COMGLYCININ, ETC.).
	CC	-----
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	CC	-----
	DR	EMBL; M24845; AAA33467.1; "-"
	DR	HSSP; P50477; ICAM.
	DR	MAIZEDB; 30181; "-"
	DR	INTERPRO: IPR001113; "-"
	DR	PFAM; PF00546; Seedstoc_7s; 1.
	KW	Seed storage protein; Signal.
	FT	SIGNAL
	FT	PROPEP
	FT	CHAIN
	FT	CARBONYD
	SQ	SEQUENCE
		OR 21 (POTENTIAL).
		GLOBULIN-1 S ALLELE.
		N-LINKED (GLCNAC...) (POTENTIAL).
		52SEIDID0A062976 CRC64;

[illegible]

```
D6      439 FVAASRSKSNQIYCFEYHADRNKEVFLAGAD-NVLQEDLRVAKALSFASKAEVEVDLG 497
QY      630 SQDSIEFFGPRQ---HQDSSRTKKQQ 655
       +-+ ++++++
Db      498 SRREKGFLPGPKESGGHEERQDEEEERE 526
```

	RESULT	4
AC	AH11_ARAHY	
ID	AH11_ARAHY	STANDARD; PRT; 614 AA.
AC	P43237;	
DT	01-NOV-1995 (Rel. 32, Created)	
DT	01-NOV-1995 (Rel. 32, Last sequence update)	
DT	01-NOV-1997 (Rel. 35, Last annotation update)	
DE	ALLERGEN ARA H 1, CLONE p17 (ARA H 1).	
OS	Arachis hypogaea (peanut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; Eudicotyledons; core eudicots; Rosidae; eurosids I;	
OC	Fabales; Fabaceae; Papilionoideae; Arachis.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CV, FLORUNNER;	
RX	MEDLINE=96013631; PubMed=7560062;	
RA	BURKS A.W., COCKRELL G., STANLEY J.S., HELM R.M., BANNON G.A.;	
RT	"Recombinant peanut allergen Ara h I expression and IgE binding in	
RL	patients with peanut hypersensitivity.";	
JL	J. Clin. Invest. 96:1715-1721(1995).	
CC	-I- SIMILARITY: TO 7S SEED STORAGE PROTEINS (PHASCOLIN, VICILIN,	
CC	CONVICILIN, CONGLYCININ, ETC.).	

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L38853; AAA60336.1; -.
DR HSSP; P50477; ICAM.
DR INTERPRO; IPR001113; -.
DR PFMAM; PF00546; Seedstore_7s; 1.
KW Allergen.
SQ SEQUENCE 614 AA; 70283 MW; 1DDACFE217EECF31 CRC64;

[illegible]


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RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-50.
RC TISSUE-EMBRYO;
RX MEDLINE-93104680; PubMed-1467654;
RA Grimes H.D., Overvoorde P.J., Rapp K., Franceschi V.R., Hiltz W.D.;
RT "A 65-kD sucrose binding protein is expressed and localized in
  tissues actively engaged in sucrose transport."
RL Plant Cell 4:1561-1574(1992).
CC -1- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
CC -1- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
  SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE
  MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF
  MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.
CC -1- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED
  UNTIL 10 DAYS AFTER FERTILIZATION, BETWEEN 10-19 DAYS AFTER
  FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
  DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO
  EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE
  RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06038; AAB03894.1; -.
DR PIR: J01730; J01730.
DR HSSP: P50477; ICAM.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore.7s; 1.
KM Transport; Sugar transport; Signal; Membrane.
PT SIGNAL
PT CHAIN 30 524 SUCROSE-BINDING PROTEIN.
SQ SEQUENCE 524 AA; 60522 MW; 0251EE90796EF341 CRC64;

Query Match 22.6%; Score 798; DB 1; Length 524;
Best Local Similarity 33.2%; Pred. No. 2.9e-42;
Matches 190; Conservative 100; Mismatches 180; Indels 102; Gaps 16;

OY 105 RCEICEEEYRNDPQ--QOYECCOERHETEPRIHQCOOQRCERREYKEREKQO 162
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 27 KCEETEVEE-----DPELVTKHCCQOQOQYTEGDKR---VCLQSCD-RYHRMKEERE 76
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 163 KRYEEOQREDEERYERKMEEDKRDPOQREYDCRRRCQEOBPRQOYOCRRRCQOQO 222
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 77 KOJOETREKKEE-ESRERE-----EQQEQ 101
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 223 HGGGGLINDQRCGSGRYEEGEEKOSDNPYDE-RSLSTRFTEGHSVLENFGRSK 281
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 102 H-----EEQDENPYTFEDKDFEYRVETEGGRVLRVLRKPFESK 140
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 282 LRLAKNYRLVLEANPNFVLPTHDADAILVTGRGALKMINDNESYVLECGDY 341
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 141 LLOGIENFRALILEARINFVSPRHFDSEVFNENINGRAVLGLVSETEKTLFEGDM 200
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 342 RIPAGCTTYLINDNNERLHA--KFLQITSTPGQYKEFPAGGONDEPYLSTFSEKILE 399
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 201 HIPAGPLIVNDENDKLFALMLHIPVSSTPGKEFEFFAPGGRDESLAFSNVILQ 260
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 400 AALNTAQRIRGLVGOOREGVIIISASOEQIRELTRDSESRMHIRGSESSGPFYNL 459
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 261 AALQTKKGLKLENFDOONESTFRISREOVRAIA-PYKSSWMPF--GGE-SKQPFNIFS 316
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 460 KRLVSNKYGOAEVKEPEYRQ--LQDMQSVYIANITOGSMGPFENRSTVAVVVASG 517
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 317 KRLTINSNGRLEVGPRDDEKSMQLRLNMLFTNITQRSMTIYNSIATIALVIOG 376
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 518 EADVEMACPHLSRGHGRGRCGRHHEEDVHYEQVKARLSKREAIIVPGHPVVFVSSGN 577
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DB 377 RGHLLQISCPHMSRSSSHSK-----HDKSSPSYHRISSDLPQWVFPVPGHPVTIASNK 431
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 578 ENLLAFGIMQNNHNFENLAGERNVLOQIEPQAMELFAARKEVEELF----- 628
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 432 ENLLMICEVNAADNKKFTFAGKD-NIVSSLDNVAELAFNPSEWNGVFLQRFLEKR 490
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 629 -----NSODESIFPPGPRHOQOOSRS 650
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 491 LIGRLYHLPHKDKKESFFPFELPREGRRA 522
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
VCIC_PEA STANDARD: PRT: 459 AA.
AC P13918;
DT 01-JAN-1990 (rel. 13, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE VICILIN PRECURSOR.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-SEEDLING;
RA Higgins T.J.V., Newbigin E.J., Spencer D., Llewellyn D.J., Craig S.;
RT "The sequence of a pea vicilin gene and its expression in transgenic
  tobacco."
RL Plant Mol. Biol. 11:683-695(1988).
[2]
RP SEQUENCE OF 27-459 FROM N.A. (CLONE PDUB9).
RC STRAIN-CV, FELTHAM F1RST.
RX MEDLINE-88326226; PubMed-3046604;
RA Watson M.D., Lambert N., Delauney A., Yarwood J.N., Crox R.R.D.,
RA Gatehouse J.A., Wright D.J., Boulter D.;
RT "Isolation and expression of a pea vicilin cDNA in the yeast
  Saccharomyces cerevisiae."
RL Biochem. J. 251:857-864(1988).
CC -1- FUNCTION: SEED STORAGE PROTEIN.
CC -1- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN
  BODIES.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 11 GENES FOR VICILIN SUBUNITS.
CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,
  CONVICILIN, CONGLYCININ, ETC.).
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CC -----
DR EMBL: X14076; CAA32239.1; -.
DR EMBL: Y00722; CAA68708.1; -.
DR PIR: S00567; S00567.
DR PIR: S08505; S08505.
DR HSSP: P50477; ICAM.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore.7s; 1.
KM Seed storage protein; Multigene family; Signal.
PT SIGNAL
PT CHAIN 29 459 VICILIN.
PT CONFLICT 375 459 V->L (IN REF. 2).
PT CONFLICT 409 409 I->V (IN REF. 2).
SQ SEQUENCE 459 AA; 52231 MW; E2FA390B95451D29 CRC64;

Query Match 21.5%; Score 760.5; DB 1; Length 459;
Best Local Similarity 37.6%; Pred. No. 5e-40;
Matches 161; Conservative 79; Mismatches 159; Indels 29; Gaps 5;

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FT CONFLICT 161 161 N -> K (IN REF. 2).
SQ SEQUENCE 445 AA; 50289 MW; 739B59CC2292EAB0 CRC64;

Query Match 19.3% Score 682.5; DB 1; Length 445;

Best Local Similarity 33.1%; Pred. NO. 3e-35;
Matches 141; Conservative 98; Mismatches 164; Indels 23; Gaps 5;

```
QY 235 GGSGRYEGEGEKQSDNPNYFEDERSLSTRFTEEGHISYLENFYGRSKLLRALKNYRLVLL 294
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 32 GGEADESEESERAGNNPYLFPSNKFLLFKNQHGSLRLQRFNEDTEKLENLRDYRVLEY 91
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 295 EANNAPVLPYTHLDADAILVTGRCALKMTHRDNRESYNLECGDVIRIPAGTFYFLINR 354
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 92 CSKPNLTLLPHHSDDLLVLEGOAILVYNPDGRDPTYKLDQGDALKIQAGTFPYFLINP 151
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 355 DNNERLHAKLFOTISIPGOVKEFFPAGGONPEPYLSTFSKEILEALINTQAERL-RGYL 413
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 152 DNMGNLILNFAITFRPRGIVEDEFLSSTKRLPSYLSAFSKNPLEASYDSPYDEIEQTL 211
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 414 GOOREGVIIISASQOIRELTRDSESRWHIRRGESSRGPNLFNKRPLYSNKYGQAYE 473
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 QEEGEGVIVKMPKQDQIEISKHAGSSRKT-----SSQDKPFNLRSDPTYSNNYGLYE 267
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 474 VKPEDYROLQDMDVSVFIANTTQGSMMGPFFNTRSTKVVVVVASGEADVEMACPRLSGRHG 533
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 268 ITPEKNSQLRDLILLNCLQMNNEGALFVPHYNSRATVILVANEGRAEVELV----- 318
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 534 GRGGRKRHEEEDVHYEOK--ARLSKREAIYVPVGHVYFVSSGNENLLFAFGINAQ 590
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 319 ----GLEOQOQOQLESQMLRKYATLSEGLIVIPSSFVALKAASDLNMV--GIGVNAE 372
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 591 NNHENFLAGRERNYLOQIEPQAMELAFAPRKEVEELFNSODESIFFPGPROHQOQSSRS 650
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Db 373 NNERNFLAGKKNENYRQIPQVSDLTFFPGSGEEVEELLENGKESYFYDGGPRHIDAGKA 432
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QY 651 TKOQOP 656
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Db 433 RRAHLP 438
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Search completed: March 1, 2001, 16:16:37
Job time: 417 sec

